

Diagram illustrating the centromeric region of chromosome 12, showing the centromeric side and telomeric side. The diagram includes markers for yUP19H6, yUP19H6L, m305, yUP21A4L, g8020, yUP11H9L, and NPR1. A scale bar indicates 5kb.

Diagram illustrating the centromeric region of chromosome 12, showing the centromeric side and telomeric side. The diagram includes markers for GAP-B, yUP19H6L, m305, yUP21A4L, g8020, yUP11H9L, g11447, and m315. A scale bar indicates 2cM.

FIG. 2A

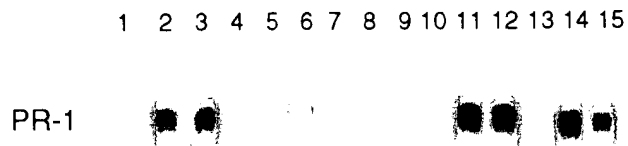


FIG. 2B

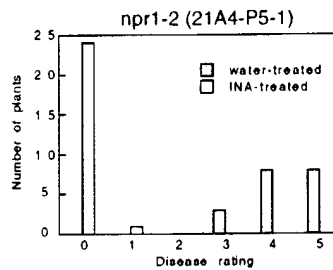
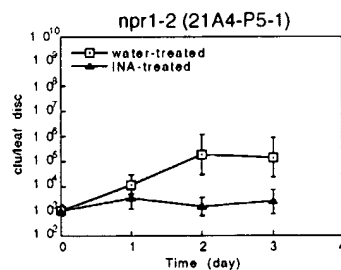
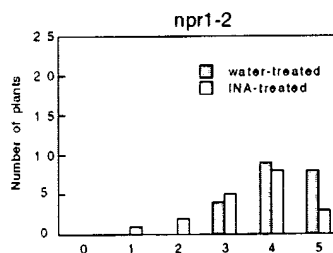
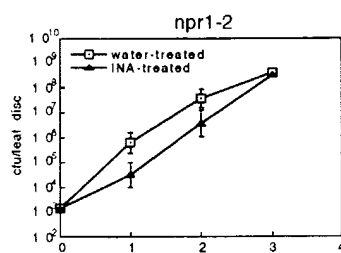
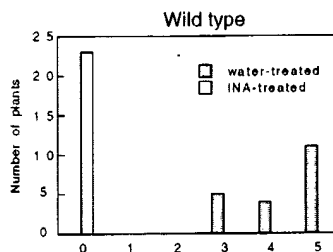
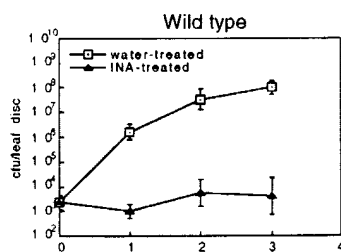
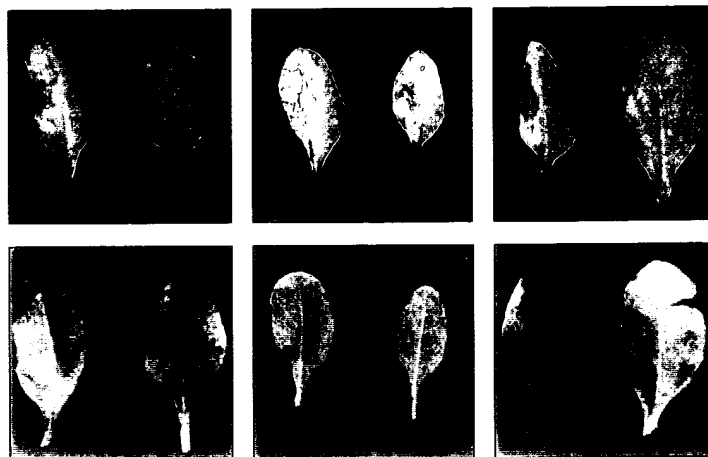


FIG. 2C

FIG. 2D

# Restriction Map of the *NPR1* Locus (7547 bp)

## Unique Sites

## Hind III and Xba I Sites

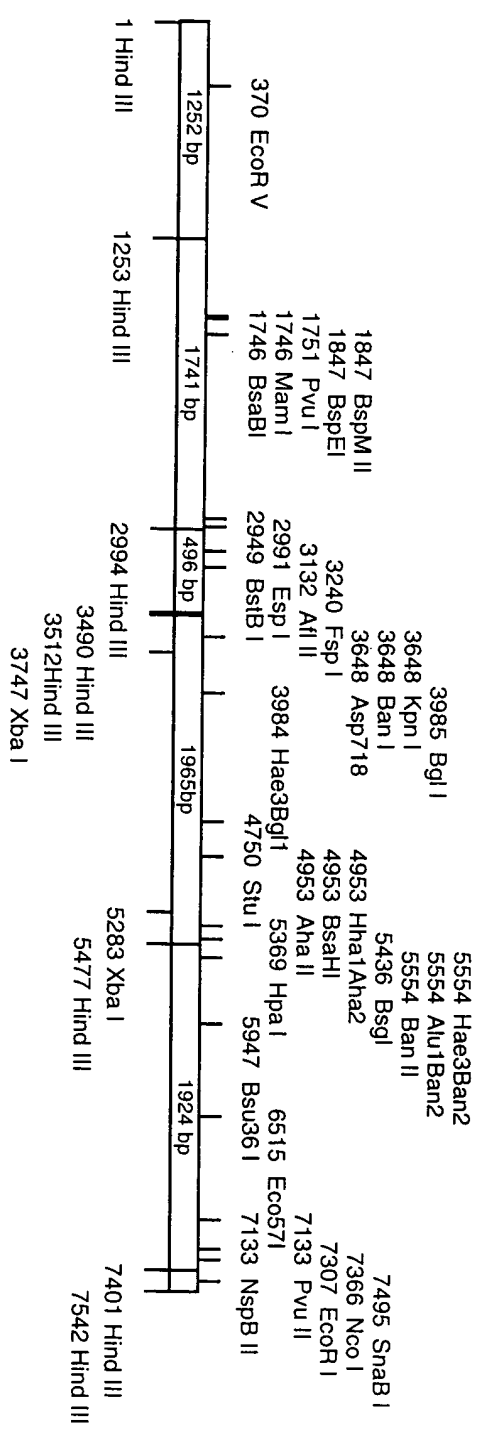


FIG. 3

03903334.030397

10	20	30	40	50
*	*	*	*	*
AAGCTTGTGA	TGCAAGTCAT	GGGATATTGC	TTTGTGTTAA	GTATACAAAA
TTCGAACACT	ACGTTTCAGTA	CCCTATAACG	AAACACAATT	CATATGTTTT
60	70	80	90	100
*	*	*	*	*
CCATCACGTG	GATACATAGT	CTTCAAACCA	ACCACTAAAC	AGTATCAGGT
GGTAGTGCAC	CTATGTATCA	GAAGTTTGGT	TGGTGATTTG	TCATAGTCCA
110	120	130	140	150
*	*	*	*	*
CATACCAAAG	CCAGAAGTGA	AGGGTTGGGA	TATGTCATTG	GGTTTAGCGG
GTATGGTTTC	GGTCTTCACT	TCCCAACCCT	ATACAGTAAC	CCAAATCGCC
160	170	180	190	200
*	*	*	*	*
TAATCGGATT	GAACCCTTTC	CGGTATAAAA	TACAAAGGCT	TTCGCAGTCT
ATTAGCCTAA	CTTGGGAAAG	GCCATATTTT	ATGTTTCCGA	AAGCGTCAGA
210	220	230	240	250
*	*	*	*	*
CGGCGTATGT	GTATGTCTCG	GGGTATCTAC	CATTTGAATC	ACAGAACTTT
GCCGCATACA	CATACAGAGC	CCCATAGATG	GTAAACTTAG	TGTCTTGAAA
260	270	280	290	300
*	*	*	*	*
TATGTGCGAA	GTTTTTCGATT	CTGATTTCGTT	TACCTGGAAG	AGATTAGAAA
ATACACGCTT	CAAAAGCTAA	GACTAAGCAA	ATGGACCTTC	TCTAATCTTT
310	320	330	340	350
*	*	*	*	*
TTTGCGTCTA	CCAAAAACAG	ACAGATTAAT	TTTTTCCAAC	CCGATACAAG
AAACGCAGAT	GGTTTTTGTC	TGTCTAATTA	AAAAAGGTTG	GGCTATGTTC
360	370	380	390	400
*	*	*	*	*
TTTCGGGGTT	CTTGCATTGG	ATATCACGGA	ACAACAATGT	GATCCGGTTT
AAAGCCCCAA	GAACGTAACC	TATAGTGCCT	TGTTGTTACA	CTAGGCCAAA
410	420	430	440	450
*	*	*	*	*
TGTCTCAAAA	CCGAAACTTG	GTCCTTCTTC	CATACTCCGA	ACTCTGATGT
ACAGAGTTTT	GGCTTTGAAC	CAGGAAGAAG	GTATGAGGCT	TGAGACTACA
460	470	480	490	500
*	*	*	*	*
TTTCTCAGGA	TTAGTCAGAT	ACGAAGGGAA	GCTAGGTGCT	ATTCGTCAGT
AAAGAGTCCT	AATCAGTCTA	TGCTTCCCTT	CGATCCACGA	TAAGCAGTCA
510	520	530	540	550
*	*	*	*	*
GGACAAACAA	AGATCAAGAA	GATGTTACAG	AGTTATGGGT	TTTAAAGAGC

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CCTGTTTGTT TCTAGTTCTT CTACAAGTGC TCAATACCCA AAATTTCTCG
      560      570      580      590      600
      *      *      *      *      *
AGTTTTGAAA AGTCGTGGGT TAAAGTGAAA GATATTAAAA GCATTGGAGT
TCAAAACTTT TCAGCACCCA ATTTCACTTT CTATAATTTT CGTAACCTCA

      610      620      630      640      650
      *      *      *      *      *
AGATTTGATT ACGTGGACTC CAAGCAACGA CGTTGTATTG TTTCGTAGTA
TCTAAACTAA TGCACCTGAG GTTCGTTGCT GCAACATAAC AAAGCATCAT

      660      670      680      690      700
      *      *      *      *      *
GTGATCGTGG TTGCCTCTAC AACATAAACG CAGAGAAGTT GAATTTAGTT
CACTAGCACC AACGGAGATG TTGTATTTGC GTCTCTTCAA CTAAATCAA

      710      720      730      740      750
      *      *      *      *      *
TATGCAAAAA AAGAGGGATC TGATTGTTCT TTCGTTTGTT TTCCGTTTGTG
ATACGTTTTT TTCTCCCTAG ACTAACAAGA AAGCAAACAA AAGGCAAAAC

      760      770      780      790      800
      *      *      *      *      *
TTCTGATTAC GAGAGGGTTG ATCTGAACGG AAGAAGCAAC GGGCCGACAC
AAGACTAATG CTCTCCCAAC TAGACTTGCC TTCTTCGTTG CCCGGCTGTG

      810      820      830      840      850
      *      *      *      *      *
TTTAAAAAAA AAATAAAAAA AATGGGCCGA CAAATGCAAA CGTAGTTGAC
AAATTTTTTT TTTATTTTTT TTACCCGGCT GTTTACGTTT GCATCAACTG

      860      870      880      890      900
      *      *      *      *      *
AAGGATCTCA AGTCTCAAGT CTCAATTGGC TCGCTCATTG TGGGGCATAA
TTCCTAGAGT TCAGAGTTCA GAGTTAACCG AGCGAGTAAC ACCCCGTATT

      910      920      930      940      950
      *      *      *      *      *
ATATATCTAG TGATGTTTAA TTGTTTTTTA TAAGGTAAAA AGGAATATTG
TATATAGATC ACTACAAATT AACAAAAAAT ATTCCATTTT TCCTTATAAC

      960      970      980      990      1000
      *      *      *      *      *
AATTTTGTTT CTTAGGTTTA TGTAATAATA CCAAACATTG TTTTATGAAT
TTAAACAAA GAATCCAAAT ACATTATTAT GGTGTGTAAC AAAATACTTA

      1010      1020      1030      1040      1050
      *      *      *      *      *
ATTTAATCTG ATTTTTTGGC TAGTTATTTT ATTATATCAA GGGTTCCTGT
TAAATTAGAC TAAAAAACCG ATCAATAAAA TAATATAGTT CCCAAGGACA

      1060      1070      1080      1090      1100
      *      *      *      *      *

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08903334-030397

TTATAGTTGA	AAACAGTTAC	TGTATAGAAA	ATAGTGTCCC	AATTTTCTCT
AATATCAACT	TTTGTC AATG	ACATATCTTT	TATCACAGGG	TTAAAAAGAGA
1110	1120	1130	1140	1150
*	*	*	*	*
CTTAAATAAT	ATATTAGTTA	ATAAAAGATA	TTTTAATATA	TTAGATATAC
GAATTTATTA	TATAATCAAT	TATTTTCTAT	AAAATTATAT	AATCTATATG
1160	1170	1180	1190	1200
*	*	*	*	*
AATAATATCT	AAAGCAACAC	ATATTTAGAC	ACAACACGTA	ATATCTTACT
TTATTATAGA	TTTCGTTGTG	TATAAATCTG	TGTTGTGCAT	TATAGAATGA
1210	1220	1230	1240	1250
*	*	*	*	*
ATTGTTTACA	TATATTTATA	GCTTACCAAT	ATAACCCGTA	TCTATGTTTT
TAACAAATGT	ATATAAATAT	CGAATGGTTA	TATTGGGCAT	AGATACAAAA
1260	1270	1280	1290	1300
*	*	*	*	*
ATAAGCTTTT	ATACAATATA	TGTACGGTAT	GCTGTCCACG	TATATATATT
TATTCGAAAA	TATGTTATAT	ACATGCCATA	CGACAGGTGC	ATATATATAA
1310	1320	1330	1340	1350
*	*	*	*	*
CTCCAAAAAA	AACGCATGGT	ACACAAAATT	TATTAAATAT	TTGGCAATTG
GAGGTTTTTT	TTGCGTACCA	TGTGTTTTAA	ATAATTTATA	AACCGTTAAC
1360	1370	1380	1390	1400
*	*	*	*	*
GGTGTTTATC	TAAAGTTTAT	CACAATATTT	ATCAACTATA	ATAGATGGTA
CCACAAATAG	ATTTCAAATA	GTGTTATAAA	TAGTTGATAT	TATCTACCAT
1410	1420	1430	1440	1450
*	*	*	*	*
GAAGATAAAA	AAATTATATC	AGATTGATTC	AATTAAATTT	TATAATATAT
CTTCTATTTT	TTTAATATAG	TCTAACTAAG	TTAATTTAAA	ATATTATATA
1460	1470	1480	1490	1500
*	*	*	*	*
CATTTTAAAA	AATTAATTAA	AAGAAAAC TA	TTTCATAAAA	TTGTTCAAAA
GTAAAATTTT	TTAATTAATT	TTCTTTTGAT	AAAGTATTTT	AACAAGTTTT
1510	1520	1530	1540	1550
*	*	*	*	*
GATAATTAGT	AAAATTAATT	AAATATGTGA	TGCTATTGAA	TTATAGAGAG
CTATTAATCA	TTTAAATTAA	TTTATACACT	ACGATAACTT	AATATCTCTC
1560	1570	1580	1590	1600
*	*	*	*	*
TTATTGTAAA	TTTACTTAAA	ATCATACAAA	TCTTATCCTA	ATTTAACTTA
AATAACATTT	AAATGAATTT	TAGTATGTTT	AGAATAGGAT	TAAATTGAAT
1610	1620	1630	1640	1650

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[illegible]

2160	2170	2180	2190	2200
*	*	*	*	*
AATATTCGAC	TTGATTTAAT	TATAGTGTA	ACATGCTGAA	CACTGAAAAT
TTATAAGCTG	AACTAAATTA	ATATCACATT	TGTACGACTT	GTGACTTTTA
2210	2220	2230	2240	2250
*	*	*	*	*
TACTTTTTCA	ATAAACGAAA	AATATAATAT	ACATTACAAA	ACTTATGTGA
ATGAAAAAGT	TATTTGCTTT	TTATATTATA	TGTAATGTTT	TGAATACACT
2260	2270	2280	2290	2300
*	*	*	*	*
ATAAAGCATG	AGACTTAATA	TACGTTCCCT	TTATCATTTT	ACTTCAAAGA
TATTTTCGTAC	TCTGAATTAT	ATGCAAGGGA	AATAGTAAAA	TGAAGTTTCT
2310	2320	2330	2340	2350
*	*	*	*	*
AAATAAACAG	AAATGTAAC	TTCACATGTA	AATCTAATTC	TTAAATTTAA
TTTATTTGTC	TTTACATTGA	AAGTGATCAT	TTAGATTAA	AATTTAAATT
2360	2370	2380	2390	2400
*	*	*	*	*
AAAATAATAT	TTATATATTT	ATATGAAAAT	AACGAACCGG	ATGAAAAATA
TTTTATTATA	AATATATAAA	TATACTTTTA	TTGCTTGGCC	TACTTTTTAT
2410	2420	2430	2440	2450
*	*	*	*	*
AATTTTATAT	ATTTATATCA	TCTCCAAATC	TAGTTTGGTT	CAGGGGCTTA
TTAAATATA	TAAATATAGT	AGAGGTTTAG	ATCAAACCAA	GTCCCCGAAT
2460	2470	2480	2490	2500
*	*	*	*	*
CCGAACCGGA	TTGAACTTCT	CATATACAAA	AATTAGCAAC	ACAAAATGTC
GGCTTGGCCT	AACTTGAAGA	GTATATGTTT	TTAATCGTTG	TGTTTTACAG
2510	2520	2530	2540	2550
*	*	*	*	*
TCCGGTATAA	ATACTAACAT	TTATAACCCG	AACCGGTTTA	GCTTCCTGTT
AGGCCATATT	TATGATTGTA	AATATTGGGC	TTGGCCAAAT	CGAAGGACAA
2560	2570	2580	2590	2600
*	*	*	*	*
ATATCTTTTT	AAAAAAGATC	TCTGACAAAG	ATTCCTTTCC	TGGAAATTTA
TATAGAAAAA	TTTTTTCTAG	AGACTGTTTC	TAAGGAAAGG	ACCTTTAAAT
2610	2620	2630	2640	2650
*	*	*	*	*
CCGGTTTTGG	TGAAATGTAA	ACCGTGGGAC	GAGGATGCTT	CTTCATATCT
GGCCAAAACC	ACTTTACATT	TGGCACCTTG	CTCCTACGAA	GAAGTATAGA
2660	2670	2680	2690	2700
*	*	*	*	*
CACCACCACT	CTCGTTGACT	GGACTTGGCT	CTGCTCGTCA	ATGGTTATCT
GTGGTGGTGA	GAGCAACTGA	CCTGAACCGA	GACGAGCAGT	TACCAATAGA

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2710	2720	2730	2740	2750
*	*	*	*	*
TCGATCTTAA	ACCAAATCCA	GTTGATAAGG	TCTCTTCGTT	GATTAGCAGA
AGCTAGAATT	TGGTTTAGGT	CAACTATTCC	AGAGAAGCAA	CTAATCGTCT
2760	2770	2780	2790	2800
*	*	*	*	*
GATCTCTTTA	ATTTGTGAAT	TTCAATTCAT	CGGAACCTGT	TGATGGACAC
CTAGAGAAAT	TAAACACTTA	AAGTTAAGTA	GCCTTGGACA	ACTACCTGTG
2810	2820	2830	2840	2850
*	*	*	*	*
CACCATTGAT	GGATTCGCCG	ATTCTTATGA	AATCAGCAGC	ACTAGTTTCG
GTGGTAACTA	CCTAAGCGGC	TAAGAATACT	TTAGTCGTCG	TGATCAAAGC
2860	2870	2880	2890	2900
*	*	*	*	*
TCGCTACCGA	TAACACCGAC	TCCTCTATTG	TTTATCTGGC	CGCCGAACAA
AGCGATGGCT	ATTGTGGCTG	AGGAGATAAC	AAATAGACCG	GCGGCTTGTT
2910	2920	2930	2940	2950
*	*	*	*	*
GTA CTCACCG	GACCTGATGT	ATCTGCTCTG	CAATTGCTCT	CCAACAGCTT
CATGAGTGGC	CTGGACTACA	TAGACGAGAC	GTTAACGAGA	GGTTGTCGAA
2960	2970	2980	2990	3000
*	*	*	*	*
CGAATCCGTC	TTTGACTCGC	CGGATGATTT	CTACAGCGAC	GCTAAGCTTG
GCTTAGGCAG	AACTGAGCG	GCCTACTAAA	GATGTCGCTG	CGATTCGAAC
3010	3020	3030	3040	3050
*	*	*	*	*
TTCTCTCCGA	CGGCCGGGAA	GTTTCTTTCC	ACCGGTGCGT	TTTGT CAGCG
AAGAGAGGCT	GCCGGCCCTT	CAAAGAAAGG	TGGCCACGCA	AAACAGTCGC
3060	3070	3080	3090	3100
*	*	*	*	*
AGAAGCTCTT	TCTTCAAGAG	CGCTTTAGCC	GCCGCTAAGA	AGGAGAAAGA
TCTTCGAGAA	AGAAGTTCTC	GCGAAATCGG	CGGCGATTCT	TCCTCTTTCT
3110	3120	3130	3140	3150
*	*	*	*	*
CTCCAACAAC	ACCGCCGCCG	TGAAGCTCGA	GCTTAAGGAG	ATTGCCAAGG
GAGGTTGTTG	TGGCGGCGGC	ACTTCGAGCT	CGAATTCCTC	TAACGGTTCC
3160	3170	3180	3190	3200
*	*	*	*	*
ATTACGAAGT	CGGTTTCGAT	TCGGTTGTGA	CTGTTTTGGC	TTATGTTTAC
TAATGCTTCA	GCCAAAGCTA	AGCCAACACT	GACAAAACCG	AATACAAATG
3210	3220	3230	3240	3250
*	*	*	*	*
AGCAGCAGAG	TGAGACCGCC	GCCTAAAGGA	GTTTCTGAAT	GCGCAGACGA

CGCGGCTTGTT

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GATGATGCGT	GTGCTCTTCA	TTTCGCTGTT	GCATATTGCA	ATGTGAAGAC
CTACTACGCA	CACGAGAAGT	AAAGCGACAA	CGTATAACGT	TACACTTCTG
3810	3820	3830	3840	3850
*	*	*	*	*
CGCAACAGAT	CTTTTAA AAC	TTGATCTTGC	CGATGTCAAC	CATAGGAATC
GCGTTGTCTA	GAAAATTTTG	AACTAGAACG	GCTACAGTTG	GTATCCTTAG
3860	3870	3880	3890	3900
*	*	*	*	*
CGAGGGGATA	TACGGTGCCT	CATGTTGCTG	CGATGCGGAA	GGAGCCACAA
GCTCCCCTAT	ATGCCACGAA	GTACAACGAC	GCTACGCCTT	CCTCGGTGTT
3910	3920	3930	3940	3950
*	*	*	*	*
TTGATACTAT	CTCTATTGGA	AAAAGGTGCA	AGTGCATCAG	AAGCAACTTT
AACTATGATA	GAGATAACCT	TTTTCACGT	TCACGTAGTC	TTCGTTGAAA
3960	3970	3980	3990	4000
*	*	*	*	*
GGAAGGTAGA	ACCGCACTCA	TGATCGCAAA	ACAAGCCACT	ATGGCGGTTG
CCTTCCATCT	TGGCGTGAGT	ACTAGCGTTT	TGTTCGGTGA	TACCGCCAAC
4010	4020	4030	4040	4050
*	*	*	*	*
AATGTAATAA	TATCCCGGAG	CAATGCAAGC	ATTCTCTCAA	AGGCCGACTA
TTACATTATT	ATAGGGCCTC	GTTACGTTTC	TAAGAGAGTT	TCCGGCTGAT
4060	4070	4080	4090	4100
*	*	*	*	*
TGTGTAGAAA	TACTAGAGCA	AGAAGACAAA	CGAGAACAAA	TTCCTAGAGA
ACACATCTTT	ATGATCTCGT	TCTTCTGTTT	GCTCTTGTTT	AAGGATCTCT
4110	4120	4130	4140	4150
*	*	*	*	*
TGTTCCCTCCC	TCTTTTGCAG	TGGCGGCCGA	TGAATTGAAG	ATGACGCTGC
ACAAGGAGGG	AGAAAACGTC	ACCGCCGGCT	ACTTAACTTC	TACTGCGACG
4160	4170	4180	4190	4200
*	*	*	*	*
TCGATCTTGA	AAATAGAGGT	ATCTATCAAG	TCTTATTTCT	TATATGTTTG
AGCTAGA A CT	TTTATCTCCA	TAGATAGTTC	AGAATAAAGA	ATATACAAAC
4210	4220	4230	4240	4250
*	*	*	*	*
AATTAAATTT	ATGTCCTCTC	TATTAGGAAA	CTGAGTGAAC	TAATGATAAC
TTAATT TAAA	TACAGGAGAG	ATAATCCTTT	GACTCACTTG	ATTACTATTG
4260	4270	4280	4290	4300
*	*	*	*	*
TATTCTTTTGT	GTCGTCCACT	GTTTAGTTGC	ACTTGCTCAA	CGTCTTTTTTC
ATAAGAAACA	CAGCAGGTGA	CAAATCAACG	TGAACGAGTT	GCAGAAAAAG
4310	4320	4330	4340	4350

* CAACGGAAGC GTTGCCTTCG	* ACAAGCTGCA TGTTTCGACGT	* ATGGAGATCG TACCTCTAGC	* CCGAAATGAA GGCTTTACTT	* GGGAACATGT CCCTTGTACA
4360 *	4370 *	4380 *	4390 *	4400 *
GAGTTCATAG CTCAAGTATC	TGACTAGCCT ACTGATCGGA	CGAGCCTGAC GCTCGGACTG	CGTCTCACTG GCAGAGTGAC	GTACGAAGAG CATGCTTCTC
4410 *	4420 *	4430 *	4440 *	4450 *
AACATCACCG TTGTAGTGGC	GGTGTAAGA CCACATTTCT	TAGCACCTTT ATCGTGGA	CAGAATCCTA GTCTTAGGAT	GAAGAGCATC CTTCTCGTAG
4460 *	4470 *	4480 *	4490 *	4500 *
AAAGTAGACT TTTCATCTGA	AAAAGCGCTT TTTTTCGCGAA	TCTAAAACCG AGATTTTGGC	GTATGGATTC CATACCTAAG	TCACCCACTT AGTGGGTGAA
4510 *	4520 *	4530 *	4540 *	4550 *
CATCGGACTC GTAGCCTGAG	CTTATCACAA GAATAGTGTT	AAAACAAAAC TTTTGTTTTG	TAAATGATCT ATTTACTAGA	TTAAACATGG AATTGTACC
4560 *	4570 *	4580 *	4590 *	4600 *
TTTTGTACT AAAACAATGA	TGCTGTCTGA ACGACAGACT	CCTTGTTTTT GGAACAAAAA	TTATCATCAG AATAGTAGTC	TGGAATCGG ACCTTGAGCC
4610 *	4620 *	4630 *	4640 *	4650 *
GAAACGATTC CTTTGCTAAG	TTCCCGCGCT AAGGGCGCGA	GTTCGGCAGT CAAGCCGTCA	GCTCGACCAG CGAGCTGGTC	ATTATGAACT TAATACTTGA
4660 *	4670 *	4680 *	4690 *	4700 *
GTGAGGACTT CACTCCTGAA	GACTCAACTG CTGAGTTGAC	GCTTGCGGAG CGAACGCCTC	AAGACGACAC TTCTGCTGTG	TGCTGAAGAA ACGACTTCTT
4710 *	4720 *	4730 *	4740 *	4750 *
ACGACTACAA TGCTGATGTT	AAGAAGCAAA TTCTTCGTTT	GGTACATGGA CCATGTACCT	AATACAAGAG TTATGTTCTC	ACACTAAAGA TGTGATTCTT
4760 *	4770 *	4780 *	4790 *	4800 *
AGGCCTTTAG TCCGGAATC	TGAGGACAAT ACTCCTGTTA	TTGGAATTAG AACCTTAATC	GAAATTCGTC CTTTAAGCAG	CCTGACAGAT GGACTGTCTA
4810 *	4820 *	4830 *	4840 *	4850 *
TCGACTTCTT AGCTGAAGAA	CCACATCGAA GGTGTAGCTT	ATCAACCGGT TAGTTGGCCA	GGAAAGAGGT CCTTCTCCA	CTAACCGTAA GATTGGCATT

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4860	4870	4880	4890	4900
*	*	*	*	*
ACTCTCTCAT	CGTCGTCGGT	GAGACTCTTG	CCTCTTAGTG	TAATTTTTGC
TGAGAGAGTA	GCAGCAGCCA	CTCTGAGAAC	GGAGAATCAC	ATTAAAAACG
4910	4920	4930	4940	4950
*	*	*	*	*
TGTACCATAT	AATTCTGTTT	TCATGATGAC	TGTAAGTGT	TATGTCTATC
ACATGGTATA	TTAAGACAAA	AGTACTACTG	ACATTGACAA	ATACAGATAG
4960	4970	4980	4990	5000
*	*	*	*	*
GTTGGCGTCA	TATAGTTTCG	CTCTTCGTTT	TGCATCCTGT	GTATTATTGC
CAACCGCAGT	ATATCAAAGC	GAGAAGCAAA	ACGTAGGACA	CATAATAACG
5010	5020	5030	5040	5050
*	*	*	*	*
TGCAGGTGTG	CTTCAAACAA	ATGTTGTAAC	AATTTGAACC	AATGGTATAC
ACGTCCACAC	GAAGTTTGTT	TACAACATTG	TTAAACTTGG	TTACCATATG
5060	5070	5080	5090	5100
*	*	*	*	*
AGATTTGTAA	TATATATTTA	TGTACATCAA	CAATAACCCA	TGATGGTGT
TCTAAACATT	ATATATAAAT	ACATGTAGTT	GTTATTGGGT	ACTACCACAA
5110	5120	5130	5140	5150
*	*	*	*	*
ACAGAGTTGC	TAGAATCAAA	GTGTGAAATA	ATGTCAAATT	GTTTCATCTGT
TGTCTCAACG	ATCTTAGTTT	CACACTTTAT	TACAGTTTAA	CAAGTAGACA
5160	5170	5180	5190	5200
*	*	*	*	*
TGGATATTTT	CCACCAAGAA	CCAAAAGAAT	ATTCAAGTTC	CCTGAAGTTC
ACCTATAAAA	GGTGGTTCTT	GGTTTTCTTA	TAAGTTCAAG	GGACTTGAAG
5210	5220	5230	5240	5250
*	*	*	*	*
TGGCAACATT	CATGTTATAT	GTATCTTCCT	AATTCTTCCT	TTAACCTTTT
ACCGTTGTAA	GTACAATATA	CATAGAAGGA	TTAAGAAGGA	AATTGGAAAA
5260	5270	5280	5290	5300
*	*	*	*	*
GTAAGTCGAA	TTACACAGCA	AGTTAGTTTC	AGGTCTAGAG	ATAAGAGAAC
CATTGAGCTT	AATGTGTCGT	TCAATCAAAAG	TCCAGATCTC	TATTCTCTTG
5310	5320	5330	5340	5350
*	*	*	*	*
ACTGAGTGGG	CGTGTAAGGT	GCATTCTCCT	AGTCAGCTCC	ATTGCATCCA
TGACTCACCC	GCACATTCCA	CGTAAGAGGA	TCAGTCGAGG	TAACGTAGGT
5360	5370	5380	5390	5400
*	*	*	*	*
ACATTTGTGA	ATGACACAAG	TTAACAATCC	TTTGCAACAT	TTCTGGGTGC
TGTAAACACT	TACTGTGTTC	AATTGTTAGG	AAACGTGGTA	AAGACCCACG

03903334 030303

FIG. 4

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FIG. 4

Sheet 12 of 14

TCCTTCTCAA TCTCTTGAC TACACACTTT TGCTGCCCTC TAATGGAACA  
AGGAAGAGTT AGAGAACATG ATGTGTGAAA ACGACGGGAG ATTACCTTGT

6510	6520	6530	6540	6550
*	*	*	*	*

CCAGTCCACC GCCTTCTTCA GTCATCCCT ATCTTTAAAA CACAACCCTA  
GGTCAGGTGG CGGAAGAAGT CGAGTAGGGA TAGAAATTTT GTGTTGGGAT

6560                  6570                  6580                  6590                  6600  
\*                      \*                      \*                      \*

CACGCAATTC ATGATCATCA ATCCACAAAC TAGACAAAGT ACACTGTTTT  
GTGCGTTAAG TACTAGTAGT TAGGTGTTTG ATCTGTTTCA TGTGACAAAA

6610	6620	6630	6640	6650
*	*	*	*	*

GAAGCACTCG AATCAACAAC ACCTTTACTT AATAAGCACG CATACGGTAA  
CTTCGTGAGC TTAGTTGTTG TGGAAATGAA TTATTCGTGC GTATGCCATT

6660	6670	6680	6690	6700
*	*	*	*	*

TACCTCTAAG CCTGGCACAT TCAAACCTTG TGTGCATCAT CTGAACCCGA  
ATGGAGATTC GGACCGTGTA AGTTTGGAAC ACACGTAGTA GACTTGGGCT

6710	6720	6730	6740	6750
*	*	*	*	*

GTTTTATCC GTTATTTCTC CATCCCCACC TCCACGAGTG CTACCATTC  
 CAAAAATAGG CAATAAAGAG GTAGGGGTGG AGGTGCTCAC GATGGTAAAG

6760                  6770                  6780                  6790                  6800  
\*                      \*                      \*                      \*                      \*

CGAAGTCAGA ATTTTCCTCG TCTTCAATCC ACCCGTTACT GTTACCCACT  
GCTTCAGTCT TAAAAGGAGC AGAAGTTAGG TGGGCAATGA CAATGGGTGA

6810	6820	6830	6840	6850
*	*	*	*	*

CCCTGAACCT CTAAACCATT ATCTCTCTCT ACTTTCACAG ATGCATGTGA  
GGGACTTGGG GATTTGGTAA TAGAGAGAGA TGAAAGTGTC TACGTACACT

6860                  6870                  6880                  6890                  6900

\*                      \*                      \*                      \*

CACATAATCA GTAGCTTCTT GGGGTTGTTG CGTCCTCTGT GTATTCGAGG  
GTGTATTAGT CATCGAAGAA CCCCAACAAC GCAGGAGACA CATAAGCTCC

6910                  6920                  6930                  6940                  6950  
\*                      \*                      \*                      \*                      \*

AACTAGCGGG ATATTCTATT ACGGATGAAC AAGCAGCATG ATCAGTAACA  
TTGATCGCCC TATAAGATAA TGCCTACTTG TTCGTCGTAC TAGTCATTGT

6960	6970	6980	6990	7000
*	*	*	*	*

TTATCAGATG TCGATTTCAC TTCCAAATAC AACTCCACAT TTCTTATAGA  
AATAGTCTAC AGCTAAAGTG AAGGTTTATG TTGAGGTGTA AAGAATATCT

7010            7020            7030            7040            7050

[illegible]



	*		*		*		*		*
AGGATGATAA	CTTGGAACCTT	CAAGCATAGT	CTCCAAACTA	GTGTCGTTCA					
TCCTACTATT	GAACCTTGAA	GTTTCGTATCA	GAGGTTTGAT	CACAGCAAGT					
7060	7070	7080	7090	7100					
*	*	*	*	*					
CTACATGAAG	AAGTAGATAG	ATAAAGAGAT	CCGGTGAAAC	AACTACAGGA					
GATGTACTTC	TTCATCTATC	TATTTCTCTA	GGCCACTTTG	TTGATGTCCT					
7110	7120	7130	7140	7150					
*	*	*	*	*					
TACTTACCAA	AATATATTGA	ACACTGATTT	CTGCAGCTGC	AATCCAAAAA					
ATGAATGGTT	TTATATAACT	TGTGACTAAA	GACGTCGACG	TTAGGTTTTT					
7160	7170	7180	7190	7200					
*	*	*	*	*					
TTGGATAAAG	ACCATTCAAC	AATGTACTTA	ACGCAGTCTT	TTGCCTAACC					
AACCTATTTC	TGGTAAGTTG	TTACATGAAT	TGCGTCAGAA	AACGGATTGG					
7210	7220	7230	7240	7250					
*	*	*	*	*					
TTGACCGTTT	TAGGAGTGGA	TCCTTCATAG	TAAACACCAT	CAGGACCATA					
AACTGGCAAA	ATCCTCACCT	AGGAAGTATC	ATTTGTGGTA	GTCCTGGTAT					
7260	7270	7280	7290	7300					
*	*	*	*	*					
CTTGGTAGAA	CCTTTCTCTC	AAGGTTTCCA	TCGCCATGAC	CATAACAGTC					
GAACCATCTT	GGAAAGAGAG	TTCCAAAGGT	AGCGGTACTG	GTATTGTCAG					
7310	7320	7330	7340	7350					
*	*	*	*	*					
CTGCAGTGAA	TTCTAAGAAA	AATGTAAAAA	ATTTTGGCCT	AAACTCATAA					
GACGTCACCT	AAGATTCTTT	TTACATTTTT	TAAACCGGA	TTTGAGTATT					
7360	7370	7380	7390	7400					
*	*	*	*	*					
TTCTTAACAT	ACGAAACCAT	GGAGAACTCC	ATGTCTAAAA	AATAAAGGCT					
AAGAATTGTA	TGCTTTGGTA	CCTCTTGAGG	TACAGATTTT	TTATTTCCGA					
7410	7420	7430	7440	7450					
*	*	*	*	*					
AAAGCTTTTT	GGCGACAGAA	GCAGATAAAT	CCATTCAAAA	CACATAAACT					
TTTCGAAAAA	CCGCTGTCTT	CGTCTATTTA	GGTAAGTTTT	GTGTATTTGA					
7460	7470	7480	7490	7500					
*	*	*	*	*					
CTAAACAATA	AACAGTGATA	CTCAATACTA	AGACTTGTA	AGGTCTACGT					
GATTTGTTAT	TTGTCACTAT	GAGTTATGAT	TCTGAACATT	TCCAGATGCA					
7510	7520	7530	7540						
*	*	*	*						
AACTCAAAAC	TGGAGAATTG	TCAGATCGGG	TGTGGCTAGT	AGAAGCTT					
TTGAGTTTTG	ACCTCTTAAC	AGTCTAGCCC	ACACCGATCA	TCTTCGAA					

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      10          20          30          40          50
      *          *          *          *          *
TCGATCTTTA ACCAAATCCA GTTGATAAGG TCTCTTCGTT GATTAGCAGA
AGCTAGAAAT TGGTTTAGGT CAACTATTCC AGAGAAGCAA CTAATCGTCT

      60          70          80          90          100
      *          *          *          *          *
GATCTCTTTA ATTTGTGAAT TTCAATTCAT CGGAACCTGT TGATGGACAC
CTAGAGAAAT TAAACACTTA AAGTTAAGTA GCCTTGGACA ACTACCTGTG
                                     M D T>

     110         120         130         140         150
     *          *          *          *          *
CACCATTGAT GGATTGCGCG ATTCTTATGA AATCAGCAGC ACTAGTTTCG
GTGGTAACTA CCTAAGCGGC TAAGAATACT TTAGTCGTCG TGATCAAAGC
      T I D   G F A   D S Y E   I S S   T S F>

     160         170         180         190         200
     *          *          *          *          *
TCGCTACCGA TAACACCGAC TCCTCTATTG TTTATCTGGC CGCCGAACAA
AGCGATGGCT ATTGTGGCTG AGGAGATAAC AAATAGACCG GCGGCTTGTT
V A T D   N T D   S S I   V Y L A   A E Q>

     210         220         230         240         250
     *          *          *          *          *
GTACTCACCG GACCTGATGT ATCTGCTCTG CAATTGCTCT CCAACAGCTT
CATGAGTGGC CTGGACTACA TAGACGAGAC GTTAACGAGA GGTTGTCGAA
V L T   G P D V   S A L   Q L L   S N S F>

     260         270         280         290         300
     *          *          *          *          *
CGAATCCGTC TTTGACTCGC CGGATGATTT CTACAGCGAC GCTAAGCTTG
GCTTAGGCAG AAAC TGAGCG GCCTACTAAA GATGTCGCTG CGATTGGAAC
      E S V   F D S   P D D F   Y S D   A K L>

     310         320         330         340         350
     *          *          *          *          *
TTCTCTCCGA CGGCCGGGAA GTTCTTTTCC ACCGGTGCGT TTTGTCAGCG
AAGAGAGGCT GCCGGCCCTT CAAAGAAAGG TGGCCACGCA AAACAGTCGC
V L S D   G R E   V S F   H R C V   L S A>

     360         370         380         390         400
     *          *          *          *          *
AGAAGCTCTT TCTTCAAGAG CGCTTTTAGCC GCCGCTAAGA AGGAGAAAAGA
TCTTCGAGAA AGAAGTTCTC GCGAAAATCGG CGGCGATTCT TCCTCTTTCT
      R S S   F F K S   A L A   A A K   K E K D>

     410         420         430         440         450
     *          *          *          *          *
CTCCAACAAC ACCGCCGCCG TGAAGCTCGA GCTTAAGGAG ATTGCCAAGG
GAGGTTGTTG TGGCGGCGGC ACTTCGAGCT CGAATTCCTC TAACGGTTCC
      S N N   T A A   V K L E   L K E   I A K>

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268980-148880580

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      460          470          480          490          500
      *            *            *            *            *
ATTACGAAGT CGGTTTCGAT TCGGTTGTGA CTGTTTTGGC TTATGTTTAC
TAATGCTTCA GCCAAAGCTA AGCCAACACT GACAAAACCG AATACAAATG
D Y E V   G F D   S V V   T V L A   Y V Y>

      510          520          530          540          550
      *            *            *            *            *
AGCAGCAGAG TGAGACCGCC GCCTAAAGGA GTTTCTGAAT GCGCAGACGA
TCGTCGTCTC ACTCTGGCGG CGGATTTCTT CAAAGACTTA CGCGTCTGCT
S S R   V R P P   P K G   V S E   C A D E>

      560          570          580          590          600
      *            *            *            *            *
GAATTGCTGC CACGTGGCTT GCCGGCCGGC GGTGGATTTC ATGTTGGAGG
CTTAACGACG GTGCACCGAA CGGCCGGCCG CCACCTAAAG TACAACCTCC
N C C   H V A   C R P A   V D F   M L E>

      610          620          630          640          650
      *            *            *            *            *
TTCTCTATTT GGCTTTCATC TTCAAGATCC CTGAATTAAT TACTCTCTAT
AAGAGATAAA CCGAAAGTAG AAGTTCTAGG GACTTAATTA ATGAGAGATA
V L Y L   A F I   F K I   P E L I   T L Y>

      660          670          680          690          700
      *            *            *            *            *
CAGAGGCACT TATTGGACGT TGTAGACAAA GTTGTTATAG AGGACACATT
GTCTCCGTGA ATAACCTGCA ACATCTGTTT CAACAATATC TCCTGTGTAA
Q R H   L L D V   V D K   V V I   E D T L>

      710          720          730          740          750
      *            *            *            *            *
GGTTATACTC AAGCTTGCTA ATATATGTGG TAAAGCTTGT ATGAAGCTAT
CCAATATGAG TTCGAACGAT TATATACACC ATTTCTGAACA TACTTCGATA
V I L   K L A   N I C G   K A C   M K L>

      760          770          780          790          800
      *            *            *            *            *
TGGATAGATG TAAAGAGATT ATTGTCAAGT CTAATGTAGA TATGGTTAGT
ACCTATCTAC ATTTCTCTAA TAACAGTTCA GATTACATCT ATACCAATCA
L D R C   K E I   I V K   S N V D   M V S>

      810          820          830          840          850
      *            *            *            *            *
CTTGAAAAGT CATTGCCGGA AGAGCTTGTT AAAGAGATAA TTGATAGACG
GAACTTTTCA GTAACGGCCT TCTCGAACAA TTTCTCTATT AACTATCTGC
L E K   S L P E   E L V   K E I   I D R R>

      860          870          880          890          900
      *            *            *            *            *
TAAAGAGCTT GGTTTGGAGG TACCTAAAGT AAAGAAACAT GTCTCGAATG
ATTTCTCGAA CCAAACCTCC ATGGATTTC TTTCTTTGTA CAGAGCTTAC
K E L   G L E   V P K V   K K H   V S N>

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2680937-1030937

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          910          920          930          940          950
          *           *           *           *           *
TACATAAGGC ACTTGACTCG GATGATATTG AGTTAGTCAA GTTGCTTTTG
ATGTATTCCG TGAAGTGAAG CTACTATAAC TCAATCAGTT CAACGAAAAC
V H K A   L D S   D D I   E L V K   L L L>

          960          970          980          990          1000
          *           *           *           *           *
AAAGAGGATC ACACCAATCT AGATGATGCG TGTGCTCTTC ATTTTCGCTGT
TTTCTCCTAG TGTGGTTAGA TCTACTACGC ACACGAGAAG TAAAGCGACA
K E D   H T N L   D D A   C A L   H F A V>

          1010         1020         1030         1040         1050
          *           *           *           *           *
TGCATATTGC AATGTGAAGA CCGCAACAGA TCTTTTAAAA CTTGATCTTG
ACGTATAACG TTACACTTCT GGC GTTGTCT AGAAAATTTT GAACTAGAAC
A Y C   N V K   T A T D   L L K   L D L>

          1060         1070         1080         1090         1100
          *           *           *           *           *
CCGATGTCAA CCATAGGAAT CCGAGGGGAT ATACGGTGCT TCATGTTGCT
GGCTACAGTT GGTATCCTTA GGCTCCCCTA TATGCCACGA AGTACAACGA
A D V N   H R N   P R G   Y T V L   H V A>

          1110         1120         1130         1140         1150
          *           *           *           *           *
GCGATGCGGA AGGAGCCACA ATTGATACTA TCTCTATTGG AAAAAGGTGC
CGCTACGCCCT TCCTCGGTGT TAACTATGAT AGAGATAACC TTTTTCACG
A M R   K E P Q   L I L   S L L   E K G A>

          1160         1170         1180         1190         1200
          *           *           *           *           *
AAGTGCATCA GAAGCAACTT TGGAAGGTAG AACCGCACTC ATGATCGCAA
TTCACGTAGT CTTCGTTGAA ACCTTCCATC TTGGCGTGAG TACTAGCGTT
S A S   E A T   L E G R   T A L   M I A>

          1210         1220         1230         1240         1250
          *           *           *           *           *
AACAAGCCAC TATGGCGGTT GAATGTAATA ATATCCCGGA GCAATGCAAG
TTGTTTCGGTG ATACCGCCAA CTTACATTAT TATAGGGCCT CGTTACGTT
K Q A T   M A V   E C N   N I P E   Q C K>

          1260         1270         1280         1290         1300
          *           *           *           *           *
CATTCTCTCA AAGGCCGACT ATGTGTAGAA ATACTAGAGC AAGAAGACAA
GTAAGAGAGT TTCCGGCTGA TACACATCTT TATGATCTCG TTCTTCTGTT
H S L   K G R L   C V E   I L E   Q E D K>

          1310         1320         1330         1340         1350
          *           *           *           *           *
ACGAGAACAA ATTCCTAGAG ATGTTCCCTC CTCTTTTGCA GTGGCGGCCG
TGCTCTTGTT TAAGGATCTC TACAAGGAGG GAGAAAACGT CACCGCCGGC
R E Q   I P R   D V P P   S F A   V A A>

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2690334-000097

[illegible]

AAAA  
TTTT

[illegible]

FIG. 6A

NPR1 (323) NHRNPRGYTVLHVAAMRKEPQLILSLLEKGAASEATLEGR TALMI AKQ (371)  
 N + GYT LH AA + +I LL+ AS +E T+ G TAL IA++  
 ankyrin 3 (740) NAKTKNGYTALHQA AQGQGH THII NVLLQNNASPNELTVNGNTALAIARR (788)

NPR1 (262) KVKKHVSNNVHKALDSDDI ELVKLL LKED (289)  
 K K +S +H A D + V+LLL+ +  
 ankyrin 3 (313) KTKNGLSPLH MATQGDHLN C VQL LLSRN (340)

FIG. 6B

1st repeat (265) KHVSNNVHKALDSDDI ELVKLL LKEDHTNLDDAC (297)  
 2nd repeat (294) DDACALHFAYAVYCNVKTATD LKLDLADVNHRN (326)  
 3rd repeat (328) RGYTVLHVAAMRKEPQLILSLLEKGAASEATL (360)  
 4th repeat (361) EGRTALMI AKQATMAVECN NIPEQCKHSLKGRL (393)

ANK consensus  
 (Michaely and Bennett) G TPLHLAAR GHVEVVKLLLD GADVNA TK  
 A I SQ NNLDIAEV K NPD D  
 V K T M R Q SI N  
 E

(Bork) t otLHhah tt thht LLt t t

10	20	30	40	50
*	*	*	*	*
GTGACTTTCT	AACATATGGCT	GAAATTGCAG	AACGAAAAAG	ACTTTCCATT
CACTGAAAGA	TTGATACCGA	CTTTAACGTC	TTGCTTTTTC	TGAAAGGTAA
60	70	80	90	100
*	*	*	*	*
TTTCACTTGA	ATGAAACCCA	AAATGGGAAAT	CTATCTCTCT	TCTTCTTCTC
AAAGTGAAC	TACTTTGGGT	TTTACCTTTA	GATAGAGAGA	AGAAGAAGAG
110	120	130	140	150
*	*	*	*	*
TTTTACTACC	TCCATTTC	TGGCTTTCCC	TCCTCTACCT	TCCCTAGCTC
AAAATGATGG	AGGTAAAGGT	ACCGAAAGGG	AGGAGATGGA	AGGGATCGAG
160	170	180	190	200
*	*	*	*	*
TTTTCAATTT	CTAGAATATT	CTTTTCTTAG	TCTGTAATTA	TCTATAGCTC
AAAAGTTAAA	GATCTTATAA	GAAAAGAATC	AGACATTAAT	AGATATCGAG
210	220	230	240	250
*	*	*	*	*
AATTTCTAAG	ACAGAACTTA	TGTAAGGCGG	CTTTCTGTAA	TGGATAATAG
TTAAAGATTC	TGTCTTGAAT	ACATTCCGCC	GAAAGACATT	ACCTATTATC
260	270	280	290	300
*	*	*	*	*
TAGGACTGCG	TTTTCTGATT	CGAATGACAT	CAGCGGAAGC	AGTAGTATAT
ATCCTGACGC	AAAAGACTAA	GCTTACTGTA	GTCGCCTTCG	TCATCATATA
310	320	330	340	350
*	*	*	*	*
GCTGCATCGG	CGGCGGCATG	ACTGAATTTT	TCTCGCCGGA	GACTTCGCCG
CGACGTAGCC	GCCGCCGTAC	TGACTTAAAA	AGAGCGGCCT	CTGAAGCGGC
360	370	380	390	400
*	*	*	*	*
GCGGAGATCA	CTTCACTGAA	ACGCCTATCG	GAAACACTGG	AATCTATCTT
CGCCTCTAGT	GAAGTGACTT	TGCGGATAGC	CTTTGTGACC	TTAGATAGAA
410	420	430	440	450
*	*	*	*	*
CGATGCGTCT	TTGCCGGAGT	TTGACTACTT	CGCCGACGCT	AAGCTTGTGG
GCTACGCAGA	AACGGCCTCA	AACTGATGAA	GCGGCTGCGA	TTCAACACCC
460	470	480	490	500
*	*	*	*	*
TTTCCGGCCC	GTGTAAGGAA	ATTCCGGTGC	ACCGGTGCAT	TTTGTGCGCG
AAAGGCCGGG	CACATTCTTT	TAAGGCCACG	TGGCCACGTA	AAACAGCCCG
510	520	530	540	550
*	*	*	*	*
AGGAGTCCGT	TCTTTAAGAA	TTTGTCTCTG	GGTAAAAAGG	AGAAGAATAG
TCCTCAGGCA	AGAAATTCTT	AAACAAGACG	CCATTTTTC	TCTTCTTATC

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560	570	580	590	600
*	*	*	*	*
TAGTAAGGTG	GAATTGAAGG	AGGTGATGAA	AGAGCATGAG	GTGAGCTATG
ATCATTCCAC	CTTAACCTCC	TCCACTACTT	TCTCGTACTC	CACTCGATAC
610	620	630	640	650
*	*	*	*	*
ATGCTGTAAT	GAGTGTATTG	GCTTATTTGT	ATAGTGGTAA	AGTTAGGCCT
TACGACATTA	CTCACATAAC	CGAATAAACA	TATCACCATT	TCAATCCGGA
660	670	680	690	700
*	*	*	*	*
TCACCTAAAG	ATGTGTGTGT	TTGTGTGGAC	AATGACTGCT	CTCATGTGGC
AGTGGATTTT	TACACACACA	AACACACCTG	TTACTGACGA	GAGTACACCG
710	720	730	740	750
*	*	*	*	*
TTGTAGGCCA	GCTGTGGCAT	TCCTGGTTGA	GGTTTTGTAC	ACATCATTTA
AACATCCGGT	CGACACCGTA	AGGACCAACT	CCAAAACATG	TGTAGTAAAT
760	770	780	790	800
*	*	*	*	*
CCTTTCAGAT	CTCTGAATTG	GTTGACAAGT	TTCAGAGACA	CCTACTGGAT
GGAAAGTCTA	GAGACTTAAC	CAACTGTTCA	AAGTCTCTGT	GGATGACCTA
810	820	830	840	850
*	*	*	*	*
ATTCTTGACA	AAACTGCAGC	AGACGATGTA	ATGATGGTTT	TATCTGTTGC
TAAGAAGTGT	TTTGACGTCG	TCTGCTACAT	TACTACCAA	ATAGACAACG
860	870	880	890	900
*	*	*	*	*
AAACATTTGT	GGTAAAGCAT	GCGAGAGATT	GCTTTCAAGC	TGCATTGAGA
TTTGTAATAA	CCATTTTCGTA	CGCTCTCTAA	CGAAAGTTCG	ACGTAACCTC
910	920	930	940	950
*	*	*	*	*
TTATTGTCAA	GTCTAATGTT	GATATCATAA	CCCTTGATAA	AGCCTTGCCCT
AATAACAGTT	CAGATTACAA	CTATAGTATT	GGGAAGTATT	TCGGAACGGA
960	970	980	990	1000
*	*	*	*	*
CATGACATTG	TAAAACAAAT	TACTGATTCA	CGAGCGGAAC	TTGGTCTACA
GTAAGTAAAC	ATTTTGTTTA	ATGACTAAGT	GCTCGCCTTG	AACCAGATGT
1010	1020	1030	1040	1050
*	*	*	*	*
AGGGCCTGAA	AGCAACGGTT	TTCTTGATAA	ACATGTTAAG	AGGATACATA
TCCCGGACTT	TCGTTGCCAA	AAGGACTATT	TGTACAATTC	TCCTATGTAT
1060	1070	1080	1090	1100
*	*	*	*	*
GGGCATTGGA	TTCTGATGAT	GTTGAATTAC	TACAAATGTT	GCTAAGAGAG

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CCCGTAACCT	AAGACTACTA	CAACTTAATG	ATGTTTACAA	CGATTCTCTC
1110	1120	1130	1140	1150
*	*	*	*	*
GGGCATACTA	CCCTAGATGA	TGCATATGCT	CTCCATTATG	CTGTAGCGTA
CCCGTATGAT	GGGATCTACT	ACGTATACGA	GAGGTAATAC	GACATCGCAT
1160	1170	1180	1190	1200
*	*	*	*	*
TTGCGATGCA	AAGACTACAG	CAGAACTTCT	AGATCTTGCA	CTTGCTGATA
AACGCTACGT	TTCTGATGTC	GTCTTGAAGA	TCTAGAACGT	GAACGACTAT
1210	1220	1230	1240	1250
*	*	*	*	*
TTAATCATCA	AAATTC AAGG	GGATACACGG	TGCTGCATGT	TGCAGCCATG
AATTAGTAGT	TTTAAGTTCC	CCTATGTGCC	ACGACGTACA	ACGTCGGTAC
1260	1270	1280	1290	1300
*	*	*	*	*
AGGAAAGAGC	CTAAAATTGT	AGTGTCCCTT	TTAACCAAAG	GAGCTAGACC
TCCTTTCTCG	GATTTTAAACA	TCACAGGGAA	AATTGGTTTC	CTCGATCTGG
1310	1320	1330	1340	1350
*	*	*	*	*
TTCTGATCTG	ACATCCGATG	GAAGAAAAGC	ACTTCAAATC	GCCAAGAGGC
AAGACTAGAC	TGTAGGCTAC	CTTCTTTTCG	TGAAGTTTAG	CGGTCTCTCCG
1360	1370	1380	1390	1400
*	*	*	*	*
TCACTAGGCT	TGTGGATTTT	AGTAAGTCTC	CGGAGGAAGG	AAAATCTGCT
AGTGATCCGA	ACACCTAAAG	TCATTCAGAG	GCCTCCTTCC	TTTTAGACGA
1410	1420	1430	1440	1450
*	*	*	*	*
TCAATGATC	GGTTATGCAT	TGAGATTCTG	GAGCAAGCAG	AAAGAAGAGA
AGCTTACTAG	CCAATACGTA	ACTCTAAGAC	CTCGTTCGTC	TTTCTTCTCT
1460	1470	1480	1490	1500
*	*	*	*	*
CCCTCTGCTA	GGAGAAGCTT	CTGTATCTCT	TGCTATGGCA	GGCGATGATT
GGGAGACGAT	CCTCTTCGAA	GACATAGAGA	ACGATACCGT	CCGCTACTAA
1510	1520	1530	1540	1550
*	*	*	*	*
TGCGTATGAA	GCTGTTATAC	CTTGAAAATA	GAGTTGGCCT	GGCTAAACTC
ACGCATACTT	CGACAATATG	GAACTTTAT	CTCAACCGGA	CCGATTGAG
1560	1570	1580	1590	1600
*	*	*	*	*
CTTTTTCCAA	TGGAAGCTAA	AGTTGCAATG	GACATTGCTC	AAGTTGATGG
GAAAAAGGTT	ACCTTCGATT	TCAACGTTAC	CTGTAACGAG	TTCAACTACC
1610	1620	1630	1640	1650
*	*	*	*	*

26090004.000000

CACTTCTGAG TTCCCACTGG CTAGCATCGG CAAAAAGATG GCTAATGCAC  
GTGAAGACTC AAGGGTGACC GATCGTAGCC GTTTTCTAC CGATTACGTG

1660 1670 1680 1690 1700  
\* \* \* \* \*

AGAGGACAAC AGTAGATTTG AACGAGGCTC CTTTCAAGAT AAAAGAGGAG  
TCTCCTGTTG TCATCTAAAC TTGCTCCGAG GAAAGTTCTA TTTTCTCCTC

1710 1720 1730 1740 1750  
\* \* \* \* \*

CACTTGAATC GGCTTAGAGC ACTCTCTAGA ACTGTAGAAC TTGGAAAACG  
TGGAACCTTAG CCGAATCTCG TGAGAGATCT TGACATCTTG AACCTTTTGC

1760 1770 1780 1790 1800  
\* \* \* \* \*

CTTCTTTCCA CGTTGTTTCCG AAGTTCTAAA TAAGATCATG GATGCTGATG  
GAAGAAAGGT GCAACAAGTC TTCAAGATTT ATTCTAGTAC CTACGACTAC

1810 1820 1830 1840 1850  
\* \* \* \* \*

ACTTGTCTGA GATAGCTTAC ATGGGGAATG ATACGGCAGA AGAGCGTCAA  
TGAACAGACT CTATCGAATG TACCCCTTAC TATGCCGTCT TCTCGCAGTT

1860 1870 1880 1890 1900  
\* \* \* \* \*

CTGAAGAAGC AAAGGTACAT GGAACCTCAA GAAATTCTGA CTAAAGCATT  
GACTTCTTCG TTTCCATGTA CCTTGAAGTT CTTTAAGACT GATTTCGTAA

1910 1920 1930 1940 1950  
\* \* \* \* \*

CACTGAGGAT AAAGAAGAAT ATGATAAGAC TAACAACATC TCCTCATCTT  
GTGACTCCTA TTTCTTCTTA TACTATTCTG ATTGTTGTAG AGGAGTAGAA

1960 1970 1980 1990 2000  
\* \* \* \* \*

GTTCCCTCTAC ATCTAAGGGA GTAGATAAGC CCAATAAGCT CCCTTTTAGG  
CAAGGAGATG TAGATTCCCT CATCTATTCTG GGTATTTCGA GGGAAATCC

2010 2020 2030 2040 2050  
\* \* \* \* \*

AAATAGGTAA TTGTATTAGG ATATATGAGG AAGAAGAGGA TTTTCTTGTA  
TTTATCCATT AACATAATCC TATATACTCC TTCTTCTCCT AAAAGAACAT

2060 2070 2080 2090 2100  
\* \* \* \* \*

ACATAGCACT CTTTCCTTTC ATCATTTGAT ATGTCAACAT ACATACAACA  
TGTATCGTGA GAAAGGAAAG TAGTAAACTA TACAGTTGTA TGTATGTTGT

2110 2120 2130 2140 2150  
\* \* \* \* \*

GCTGTACCAT AAACCTGTAT TGTGCACTT ACAACTTTGA AGAACAGAAT  
CGACATGGTA TTTGAACATA ACAACGTGAA TGTTGAAACT TCTTGTCTTA

2160 2170

25900004-00000000

TTATTTGAAA AAAAAAAAAA AA  
AATAAACTTT TTTTTTTTTT TT

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TKAFTEDKEYDKTNNISSSCSSTSKGVDPKNKLPFRK

FIG. 8A

Dosage effect of NPR1 on Psm ES4326 resistance

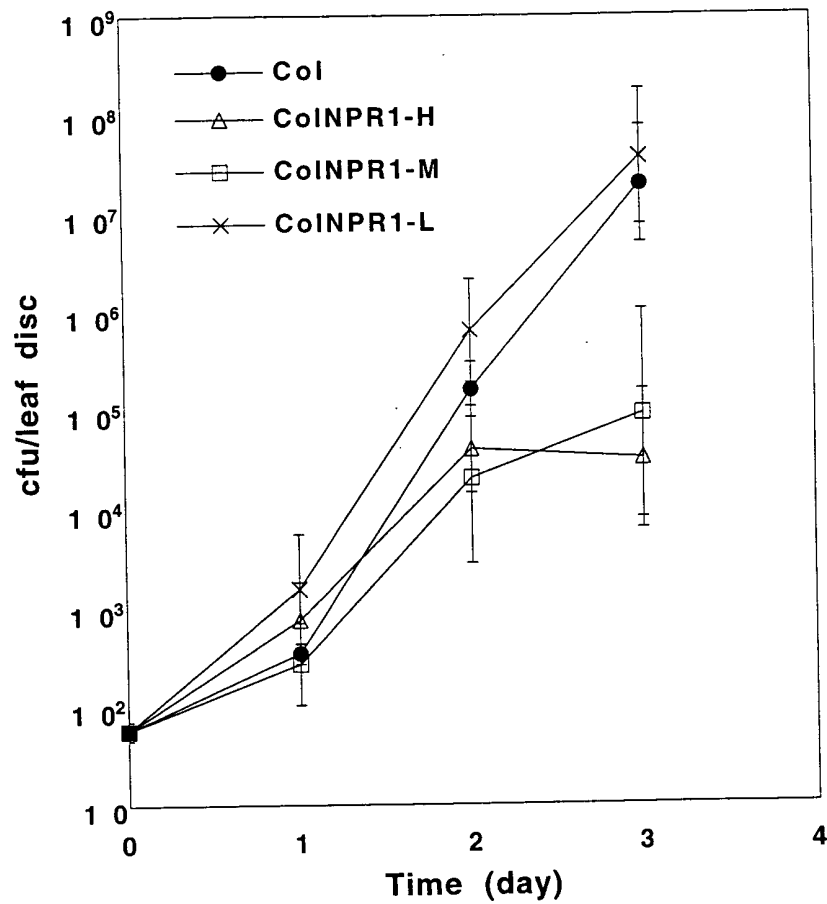
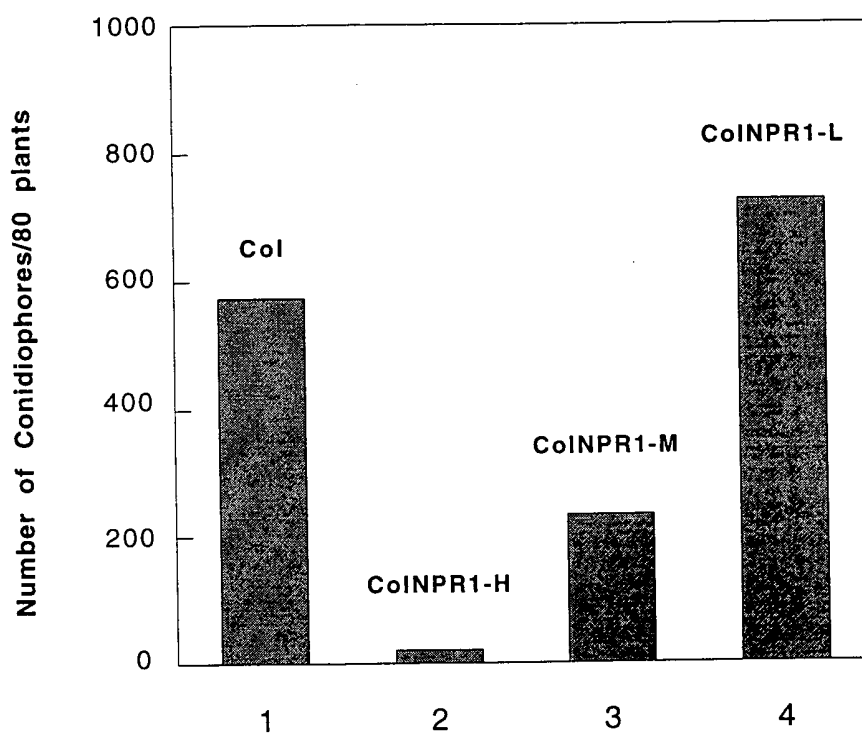


FIG. 8B

Dosage effect of NPR1 on growth of *P. parasitica*



453030-14000600

FIG. 9A

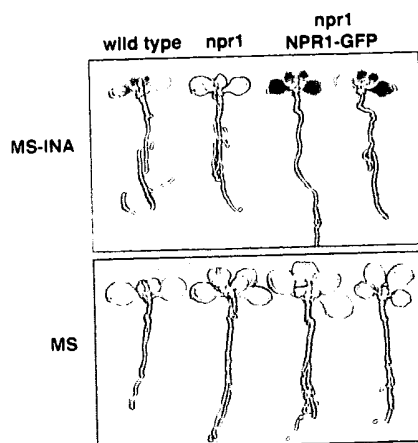


FIG. 9B

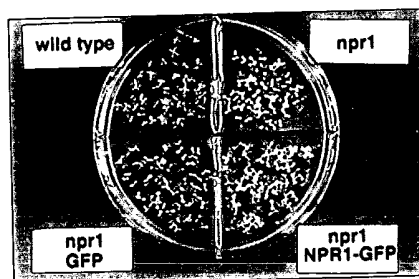


FIG. 9C

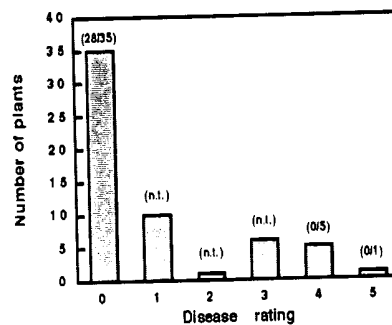
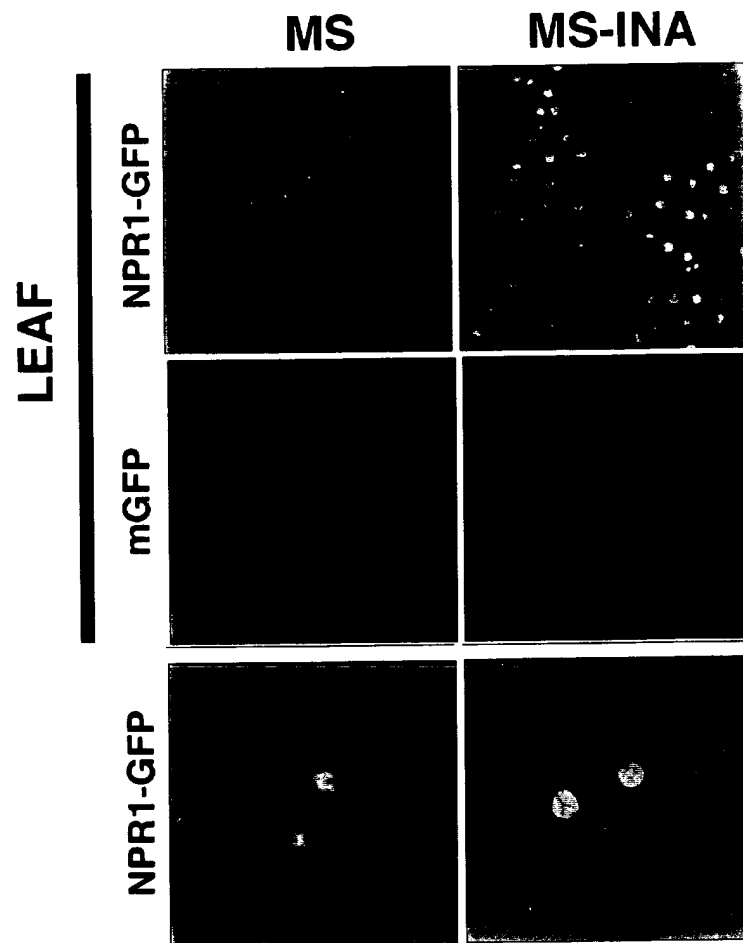




FIG. 10



FIGS. 11A-11G



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